Amendments to the claims:

Please amend the claims as shown below.

1. (Currently Amended) A composition comprising a substantially purified AvillI peptide with cellulase activity and, said AvillI peptide comprising a catalytic domain of a glycosyl hydrolase family 74- (GH74_Ace) enzyme having at least 70 90% identity to SEQ ID NO. 1, said AvillI peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74 Ace) enzyme and a carbohydrate binding domain (CBD) III., the catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to Aspergillus aculeatus Avicelase III (AviIII-Aae):

A viIII_Aac ———	DYACHRECHTURGCAGDDYF TIALCONFOCTHURDYAASTSTCTCAVALSADCDT
GII74_Acc	
AviIII_Aac	TVKCLAVGIBEMAVIGLITPPOCRALLSAVCDDCCFYHSDLDAAFNQAYHTPTVCTTNCI
GH?4_Acc	HIAPWYKGLESTAVNDLIGPPGGAPLIGALCDLCCFTHADVTAVPSTIFTSPVFTTCT8V
	Constitution of the contract o
GH74_Acc	AGPWL/TPGVQPNPPVPGPKLCMMDEMAIDPFREDMLYCTGATLYATNDLTKWGGGGGI
Aviiii_Aac	GYGGLGVDLQVPGTLMVALMCHHPDELIFRETDECATWGPIWSWNGYPGINYYYGYDIG
CH74_Ace	CYSCLTIDRQUIPNTIMVATQISWAPDTIIFROTDOGATWIRIWDWISYPARSLRYVLDIS
TIVELET TAKE	CIDINOVEDENDE CITATION CONTROL
CH74_Acc	— CPIPHKGVPDPVNIVLYIATCHTCCPYCC8SCDWKF8VTSGT#TRISPVP8TDTAM9\P GPLPHKGVLOPBSKTLYIGYANCAGPYCCTNGT/AKYNITSGU#TDISP TGLAGTYY
AvilH_Aao	T - YTSDPYGIAWYTFDETEGGGGGATTRIFYGVADAGKGYFKGEDAGATHAWYSGEPQ¥
GH74_Acc	TIGYQGDIQCVVMVAFDK8666LCQA6KTIFVCVADFNNPVFWGRDGGATHQAVFGAF T
	CNMPCHCMCGRLAVDPHQVGILYFGARGGHGLWRGTDYGATMSNVTSFTNTCTYFQD866
GII74_Acc	CHMPCRCMCERLAVOFNEDBILLYPGAPOGKGLWROTDGGATMGQMTHPPDVCTYIANPTD
AVAIII_AGC	NOTWHENCIDALATEPVETERVIVAVCMYTNEMERNVGGILRCTEGGETWFEFKLPFKVG
CH74_Acc	WRINGYNGWYCIAADPINTHKWNAAVGMYTHSWDPHDGAILRSSDQOATWQITPLPFKLG
NATILI ADC	ALGANTWONVALCACO TYDOTYINGGARGILIVRIDICGANALGAMGAWITLLDWYG ALGANTWONVYTGGGGGTTPCIVRNPGARGVANARTDICGANALGAD TWTPLHDWYG

GH74_Aee	FWAPEDPGQPVVYAVGFCNEWAA5QGVPANAQIRBDRVNPKTFYALCNCTFYRETDOGV VLLMSETSCALVSKCQC TUTAWGSLPSCAVIAEDKCDNTVPYGGGACAIYVSKNTAT
CH74_Acc	TPQPVAAGLPSSCAVGVMFHAVPCKECDLWLAASEGLYHSTNGGSSWGAI TCVSSAVNV
AVIIII_Aao	SPIRITUD LESSITUMAIR AMPEIACOVWACTDKGLAMETDYCSTFIGICSCVIACHCF
CH74_AGG	
AVIII-AAO	CFGKAEGTGGYVVIYGFPTIDGAAGLFKDEDAGTNWQVIGDAGKGFCGGGARVVNGDLQT
6 1174_Age	LRRVVICTNCRGIVYCDICCAPSC
AvilII_Aac	YCRVFRCHERPCHLLRQCQREPAC

- (Previously Presented) The composition of claim 1 wherein the
 Avilli peptide is further defined as comprising a linker and a signal sequence.
 - 3. (Cancelled)
- 4. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 80 to about 150 amino acids.
- 5. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the Avilli peptide is further defined as comprising a length of about 90 amino acids.
- 6. (Previously Presented) The composition of claim 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide sequence identical to SEQ ID NO: 3.
- 7. (Previously Presented) The composition of claim 1 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 4.
- 8. (Previously Presented) The composition of claim 1 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.
- 9. (Previously Presented) The composition of claim 1 wherein said Avilli protein comprises sequences identical to the polypeptides of SEQ ID NO: 3 and SEQ ID NO: 4.

- 10. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74_Ace has at least 90% sequence identity with SEQ ID NO: 3.
- 11. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74 has at least 80% sequence identity with SEQ ID NO: 3.
- 12. (Previously Presented) An isolated AvilII peptide having a polypeptide sequence of SEQ ID NO: 1.
 - 13. (Cancelled)
- 14. (Previously Presented) An industrial mixture suitable for degrading cellulose, such mixture comprising the AvillI polypeptide of claim 1.
- 15. (Currently Amended) The industrial mixture of claim 14 further defined as comprising a detergent,[.]
 - 16-27 (Cancelled)
- 28. (Previously Presented) An isolated polypeptide molecule comprising at least one polypeptide sequence selected from the group consisting of:
 - a) a polypeptide sequence of SEQ ID NO: 3:
 - b) a polypeptide sequence of SEQ ID NO: 4;
 - c) a polypeptide sequence of SEQ ID NO: 5;
 - d) a polypeptide sequence of SEQ ID NO: 1; and
 - e) combinations thereof.
 - 29. (Cancelled)
- 30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.
- 31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

- 32. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.
- 33. (Previously Presented) The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemaglutinin, glutathione S-tranferase, or OmpA signal sequence tag.
- 34. (Original) The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.
- 35. (Original) The fusion protein of claim 34, wherein the agent is a leucine zipper.
- 36. (Original) A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 28 bound to cellulose.

37-42 (Cancelled)

43. (Original) A composition comprising the polypeptide molecule of claim 28 and a carrier.

44-46. (Cancelled)

47. (New) The composition of claim 1 wherein said catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AviIII_Aac):

GH74_Ace	attqpytwsmvaigggg-fvdgivfnegapgilyvrtdiggmyrwdaangrwiplldwvg
AviIII Aac	aasqaytyknyvtgggggftpgivfnpsakgvayartdiggayrlnsdd-twtpimdwyg
_	
GH74 Ace	wnnwgyngvvsiaadpintnkvwaavgmytnswdpnegailrssd@gatw@itplpfklg
AviIII_Aac	NDTWHDWGIDALATDFVDTDRVYVAVGMYTNEWDFNVGSILRSTDQGDTWTETKLPFKVG
GH74_Ace	gnmpgrengerlavdpnnunilyfgapsgkelwrstdsgatwsqmtnfpdvgty1anptd
AviIII Aac	GNMPGRGMGERLAVDPNKNEILYFGARSGHGLWKSTDYGATWSMVTSFTWTGTYFODSSS

GH74 Ace	TTGYQSDIQGVVWVAFDKSSSSLGQASKTIFVGVADPNNPVFWSRDGGATWQAVPGAP-T
AVIIII ABC	TYTSDPVGIAWVTFDSTSGSSGSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY
<u>-</u>	* * * * *; **; **; * * * * * * * * * *
GH74_Ace	GPIPHKGVFDPVNHVLYIATSNTGGPYDGSSGDVWKFSVTSGTWTRISPVPSTDTANDYF
AviIII Aac	GFLPHKGVLSPEEKTLYI SYANGAG PYDGTNGTVHKYN I TSGVWTDI SPTSLASTYY
_	- v#:#####::# ::::###::# .#####::# # #:::###;## ### - #, #, #;

GH74_Ace	GYSGLTIDRQHPNTIMVATQISHWPDTIIFRSTDGGATWTRIWDWTSYPNRSLRYVLDIS
AviIII_Aac	GYGGLSVDLQVPGTLMVAALNCHWPDBLIFRSTDSGATWSPIWEWNGYPSINYYYSYDIS
GH74_Ace AviIII_Aac	AEPWLTFGVQPNPPVPSPKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTKWDSGGQI NAFWIQDTTSTDQFPVRVGWMVEALAIDPFDSNHWLYGTGLTVYGGHDLTNWDSKMNV **:: ::*** **:*****; **** *:* :****** ;:
GH74_ACB AviIII_Aac	HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSV TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLDAAPNQAYHTPTYGTTNGI *.** ** .**.**.**.**.**.**.**.**.**.
GH74_Ace	DYAELNPSIIVRAGEFDPSSQPNDRHVAFSTDGGKNWFQGSEPGGVTTGGTVAASADGSR
AviIII_Aac	DYAGNKPSNIVRSGASDDYPTLALSSNFGSTWYADYAASTSTGTGAVALSADGDT
GH74_Ace	FVWAPGDPGQPVVYAVGPGNSWAASQGVPANAQIRSDRVNPKTFYALGNGTFYRSTDGGV
AviIII_Aac	VLLMSSTSGALVSKSQGTLTAVSSLPSGAVIASDKSDNTVFYGGSAGAIYVSKNTAT
GH74_Ace AviIII_Aac	TPOPVAAGLPSSGAVGVMFHAVPGKEGDLMLAASSGLYHSTNGGSSWSAI-TGVSBAVNV SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTOIGSGVTAGWSF :* * ** :* ** : * ** : * ** : * * * *
GH74_Ace	GFGK8APGSSYPAVFVVGTIGGVTGAYRBDDCGTTWVLINDDQHQYGN-WGQAITGDHAN
AviIII_Aac	GFGKASSTGSYVVIYGFFTIDCAAGLPKSEDAGTNWQVISDABHGFGSGSANVVMGDLQT
GH74_Ace AviIII_Aac	LRRVYIGTMCRGIVYCDIGGAPSG YGRVFRGHERPGHLLRQSQREPAG **: * : * : * : * : * : * : * : * : * :

- 48. (New) The composition of claim 47 wherein said Avilli peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.
- 49. (New) A composition comprising a substantially purified AviIII peptide having at least 99% identity to SEQ ID NO. 1, said AvilII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III.
- 50. (New) The composition of claim 49 wherein said catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to Aspergillus aculeatus Avicelase III (AviIII_Aac):

GH74_Ace	ATTOPYTWONVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPLLDWVG
AviIII_Aac	AASOAYTWKNVVTGGGGGPTPGIVFNPBAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG
GH74_Ace	WNNWGYNGVVSIAADPINTNKVWAAVGHYTNSWDPNDQAILRSSDQGATWQITPLPPKLG
AviIII_Aac	NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSILRSTDQGDTWTETKLPPKVG
GH74_Ace	GNMPGRGMGERLAVDPNNDNILYFGAPEGKGLWRETDEGATWSQMTNPPDVGTYIANPTD
AviIII_Aac	GNMPGRGMGERLAVDPNKNSILYFGAREGHGLWKSTDYGATWSNVTSPTWTGTYPQDSSS

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GH74_Ace AviIII_Aac	TTGYQSDIQGVVWVAFDKSSSSLGQASKTIFVGVADPMNPVFWSRDGGATWQAVPGAP-T TYTSDPVGIAWVTFDSTSGSSGSATPRIFVGVADAGKEVFKSEDAGATWAWVSGEPQY * ** *: .**:**.:* *.* *.**
GH74_ACE	GFIPHKGVFDPVNHVLYIATSNTGGPYDGSSGDVMKFSVTSGTWTRISPVPSTDTANDYF
AVIIII_Aac	GFLPHKGVLSPEBKTLYISYANGAGPYDGTNGTVHKYNITSGVWTDISPTSLASTYY
GH74_Ace	GYSGLTIDRQHPNTIMVATQISMWPDTIIFRSTDGGATWTRIWDWTSYPNRSLRYVLDIS
AviIII_Aac	GYGGLSVDLQVPGTLMVAALNCWWPDELIFRSTDSGATWSPIWEWNGYPSINYYYSYDIS
GH74_Ace AviIII_Aac	AEPWLTFGVQPNPPVP3PKLGWMDRAMAIDPFNSDRMLYGTGATLYATNDLTKWD3GGQI NAPWIQDTTSTDQFPVRVGWMVEALAIDPFD3NHWLYGTGLTVYGGHDLTNWD5KHNV **:: ::*** **:******; **** *:* ::*** ::
GH74_Ace AviIII_Aac	HIAPMVKGLRETAVNDLİSPPSGAPLISALGDLGGPTHADVTAVPSTIFTSPVFTTGTSV TVKSLAVGIREMAVLGLITPPGGPALLSAVGNDGGFYHSDLDAAPNQAYHTPTYGTTNGI * . * . * . * . * . * . * . * . *
GH74_Ace	DYAELNPSIIVRAGSFDPSSQPNDRHVAFSTDGGKNWFQGSEPGGVTTGGTVAASADGSR
AviIII_Aac	DYAGNKPSNIVRSGASDDYPTLALSSNFGSTWYADYAASTSTGTGAVALSADGDT
GH74_Ace	FVWAPGDEGQPVVYAVGFGNSWAASQGVPANAQIRSDRVNPKTFYALSNGTFYRSTDGGV
AviIII_Aac	VLLMSSTSGALVSK8QGTLTAVESLPSGAVIASDKEDNTVFYGGSAGAIYVSKNTAT
GH74_Ace AviIII_Aac	TFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV SFTKTVS-LGSSTTVNAIR-AHPSLAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF .* * ** : *
GH74_Ace	GFGKBAPGSSYPAVFVVGTIGGVTGAYRSDDCGTTWVLINDDQMQYGN-WGQAITGDHAN
AviIII_Aac	GFGKASSTGSYVVIYGFFTIDGAAGLFKSEDAGINWQVIEDASHGFGSGSANVVNGDLQT
GH74_Ace AviIII_Aac	LRRVYIGTNGRGIVYGDIGGAPSG YGRVFRGHERPGHLRQSQREPAG **: * ; *:*

- 51. (New) The composition of claim 50 wherein said AviIII peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.
- **52**. (New) A composition comprising a substantially purified AvillI peptide having an amino acid sequence identical to SEQ ID NO. 1, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III.
- 53. (New) A composition comprising a substantially purified AviIII peptide, said AvillI peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III, said catalytic domain GH74_Ace having a sequence that is at least 90% identical to SEQ ID NO. 3.

(New) The composition of claim 51 wherein said catalytic domain 54. GH74_Ace has a sequence identical to SEQ ID NO. 3.